



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 9

TO: Robert Mondesi
Location: cm-1/5d169b01
Art Unit: 1653
Friday, June 27, 2003

Case Serial Number: 832501

From: Toby Port
Location: Biotech-Chem Library
CM1-6A04
Phone: 308-3534

toby.port@uspto.gov

Search Notes

Dear Examiner Mondesi,

Here are the results of your search.
Please feel free to contact me if you have any questions.

Toby Port



STIC SEARCH RESULTS FEEDBACK FORM

Biotech-Chem Library

Questions about the scope or the results of the search? Contact *the searcher or contact:*

Mary Hale, Information Branch Supervisor
308-4258, CM1-1E01

Voluntary Results Feedback Form

➤ I am an examiner in Workgroup: Example: 1610

➤ Relevant prior art **found**, search results used as follows:

- ☐ 102 rejection
- ☐ 103 rejection
- ☐ Cited as being of interest.
- ☐ Helped examiner better understand the invention.
- ☐ Helped examiner better understand the state of the art in their technology.

Types of relevant prior art found:

- ☐ Foreign Patent(s)
- ☐ Non-Patent Literature
(journal articles, conference proceedings, new product announcements etc.)

➤ Relevant prior art **not found**:

- ☐ Results verified the lack of relevant prior art (helped determine patentability).
- ☐ Results were not useful in determining patentability or understanding the invention.

Comments:

Drop off or send completed forms to STIC/Biotech-Chem Library, CM1 – Circ. Desk



The first part of the paper discusses the importance of the study and the objectives of the research. It highlights the need for a comprehensive understanding of the subject matter and the role of the researcher in this process. The second part of the paper presents the methodology used in the study, including the data collection methods and the analysis techniques. The third part of the paper discusses the results of the study and the conclusions drawn from the findings. The final part of the paper provides a summary of the key points and offers suggestions for further research.

The study was conducted in a systematic and rigorous manner, following the principles of scientific research. The data was collected from a large sample of participants, ensuring the representativeness of the findings. The analysis was performed using advanced statistical techniques, allowing for a detailed examination of the data. The results of the study are presented in a clear and concise manner, highlighting the key findings and their implications.

The findings of the study have significant implications for the field of research. They provide a new perspective on the subject matter and offer valuable insights into the underlying mechanisms. The study also identifies areas for further research, suggesting that the current findings are a starting point for a more in-depth exploration of the topic.

In conclusion, the study has successfully achieved its objectives and has provided a comprehensive understanding of the subject matter. The findings are robust and reliable, and they have the potential to contribute to the advancement of the field. The study also highlights the importance of a systematic and rigorous approach to research, and it offers suggestions for future research in this area.

From: Mondesi, Robert
Sent: Thursday, June 26, 2003 3:18 PM
To: STIC-Biotech/ChemLib
Subject: sequence search

My Name Robert Mondesi
ART UNIT is 1653
Phone # 305-4445
Room number 5D16
Examiner number 79912.

please perform a sequence search on SEQ ID NO : 18 of patent number 09832501.

Thank you.



[illegible]

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[illegible]

in a study with both methods. These data are presented in Table 1. The results show that the two methods are in good agreement, with the difference being statistically not significant ($P > 0.05$).

[illegible]

[illegible][illegible]

Report generated by:

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Protein: protein search using SW model

File: out June 27, 2003, 17:29:19 Search time: 14 seconds

(without alignment)

278,154 million cell updates/sec

13 foot

protein search

Sequence

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Foot. No. is the number of footprints produced by chance to have a score greater than or equal to the score of the result point printed and is derived by analysis of the total score distribution.

SUMMARY

Footprint	Score	Match	Length	DB	Description
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5	41.8	100%	600	1	serum albumin, from
6	41.8	100%	600	1	serum albumin, from
7	41.8	100%	600	1	serum albumin, from
8	41.8	100%	600	1	serum albumin, from
9	41.8	100%	600	1	serum albumin, from
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Database version 5.1.1
Copyright (c) 1998-2003 Compugen Ltd.

db protein protein search using SW model

run date: June 27, 2003, 16:50:55 : Search time 26 seconds
(without alignment)

970,641 Million cell of hits/sec

11,000
protein score 4103

Sequence: 1 LAHGVVAVHKK:HEHRE.....LVAHREKELVALGNNR:PGV

Sequence: protein062
Group: 10.0 : Expect 0.5

Score: 11,000 seqs, 4147,628 residues

1 hit number of hits satisfying chosen parameters: 11,000

Minimum job seq length: 0

Maximum job seq length: 20000000

1 seq 11 crosses: Maximum Match 100%

Database: SwissProt 401*

Note: Now in the number of results produced by chance to have a score greater than or equal to the score of the length being filtered, and is derived by analysis of the total score distribution.

SEQUENCES

Result	No.	Score	Match	Length	Hit	Description
1	1	100.0	100.0	100	1	ALBU_HUMAN
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3	3	99.8	99.8	100	1	ALBU_HUMAN
4	4	99.7	99.7	100	1	ALBU_HUMAN
5	5	99.6	99.6	100	1	ALBU_HUMAN
6	6	99.5	99.5	100	1	ALBU_HUMAN
7	7	99.4	99.4	100	1	ALBU_HUMAN
8	8	99.3	99.3	100	1	ALBU_HUMAN
9	9	99.2	99.2	100	1	ALBU_HUMAN
10	10	99.1	99.1	100	1	ALBU_HUMAN
11	11	99.0	99.0	100	1	ALBU_HUMAN
12	12	98.9	98.9	100	1	ALBU_HUMAN
13	13	98.8	98.8	100	1	ALBU_HUMAN
14	14	98.7	98.7	100	1	ALBU_HUMAN
15	15	98.6	98.6	100	1	ALBU_HUMAN
16	16	98.5	98.5	100	1	ALBU_HUMAN
17	17	98.4	98.4	100	1	ALBU_HUMAN
18	18	98.3	98.3	100	1	ALBU_HUMAN
19	19	98.2	98.2	100	1	ALBU_HUMAN
20	20	98.1	98.1	100	1	ALBU_HUMAN
21	21	98.0	98.0	100	1	ALBU_HUMAN
22	22	97.9	97.9	100	1	ALBU_HUMAN
23	23	97.8	97.8	100	1	ALBU_HUMAN
24	24	97.7	97.7	100	1	ALBU_HUMAN
25	25	97.6	97.6	100	1	ALBU_HUMAN
26	26	97.5	97.5	100	1	ALBU_HUMAN
27	27	97.4	97.4	100	1	ALBU_HUMAN
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29	29	97.2	97.2	100	1	ALBU_HUMAN
30	30	97.1	97.1	100	1	ALBU_HUMAN
31	31	97.0	97.0	100	1	ALBU_HUMAN
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34	34	96.7	96.7	100	1	ALBU_HUMAN
35	35	96.6	96.6	100	1	ALBU_HUMAN
36	36	96.5	96.5	100	1	ALBU_HUMAN
37	37	96.4	96.4	100	1	ALBU_HUMAN
38	38	96.3	96.3	100	1	ALBU_HUMAN
39	39	96.2	96.2	100	1	ALBU_HUMAN
40	40	96.1	96.1	100	1	ALBU_HUMAN
41	41	96.0	96.0	100	1	ALBU_HUMAN
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43	43	95.8	95.8	100	1	ALBU_HUMAN
44	44	95.7	95.7	100	1	ALBU_HUMAN
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73	73	92.8	92.8	100	1	ALBU_HUMAN
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80	80	92.1	92.1	100	1	ALBU_HUMAN
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83	83	91.8	91.8	100	1	ALBU_HUMAN
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86	86	91.5	91.5	100	1	ALBU_HUMAN
87	87	91.4	91.4	100	1	ALBU_HUMAN
88	88	91.3	91.3	100	1	ALBU_HUMAN
89	89	91.2	91.2	100	1	ALBU_HUMAN
90	90	91.1	91.1	100	1	ALBU_HUMAN
91	91	91.0	91.0	100	1	ALBU_HUMAN
92	92	90.9	90.9	100	1	ALBU_HUMAN
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80	1.29	1.29	1.29	1	ALBU_HUMAN
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82	1.29	1.29	1.29	1	ALBU_HUMAN
83	1.29	1.29	1.29	1	ALBU_HUMAN
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85	1.29	1.29	1.29	1	ALBU_HUMAN
86	1.29	1.29	1.29	1	ALBU_HUMAN
87	1.29	1.29	1.29	1	ALBU_HUMAN
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90	1.29	1.29	1.29	1	ALBU_HUMAN
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93	1.29	1.29	1.29	1	ALBU_HUMAN
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95	1.29	1.29	1.29	1	ALBU_HUMAN
96	1.29	1.29	1.29	1	ALBU_HUMAN
97	1.29	1.29	1.29	1	ALBU_HUMAN
98	1.29	1.29	1.29	1	ALBU_HUMAN
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100	1.29	1.29	1.29	1	ALBU_HUMAN

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61 "The human alpha-fetoprotein gene. Sequence organization and the 5'
 62 flanking region." J. Biol. Chem. 260:5055-5060(1985).
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1  COUNTRY: USA
2  FILE: 19426
3  REPORTER: REANALYST: DARR
4  MEDIUM TYPE: Floppy disk
5  COMPUTER: Motorola
6  OPERATING SYSTEM: System 7.1
7  SUBJECT: Wood 5.0 (1942610)
8  SUBJECT: ANALYST: N. LATA.
9  ANALYST: N. LATA.
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